SEQUENCE LISTING

<110> UNIVERSITE CATHOLIQUE DE LOUVAIN
       UNIVERSITE DE MONS-HAINAUT

<120> Peroxisome-associated polypeptide, nucleotide sequence encoding
       said polypeptide and their uses in the diagnosis and/or treatment
       of lung injuries and diseases, and of oxidative stress-related
       disorders

<130> DECLE30.001CP1

<140> US 10/686,157
<141> 2003-10-15

<150> US 6,759,194
<151> 2000-08-15

<150> PCT/BE98/00124
<151> 1998-08-20

<150> BE 1011331
<151> 1997-08-20

<160> 21

<170> PatentIn version 3.3

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gaaggggagc cagggaacaa ggtgaacctg gcagagctgt tcaagggcaa gaagggtgtg   300

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atagtgaagg ccctgaatgt ggaaccagat ggcacaggcc tcacctgcag cctggcaccc   660

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                20                  25                  30


Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe Thr Pro Gly Cys
            35                  40                  45


Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Glu Ala Leu Lys
        50                  55                  60


Ala Lys Gly Val Gln Val Val Ala Cys Leu Ser Val Asn Asp Ala Phe
65                  70                  75                  80


Val Thr Gly Glu Trp Gly Arg Ala His Lys Ala Glu Gly Lys Val Arg
                85                  90                  95


Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu Thr Asp Leu Leu
            100                 105                 110


Leu Asp Asp Ser Leu Val Ser Ile Phe Gly Asn Arg Arg Leu Lys Arg
            115                 120                 125


Phe Ser Met Val Val Gln Asp Gly Ile Val Lys Ala Leu Asn Val Glu
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Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro Asn Ile Ile Ser
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Gln Leu
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agtgccgcgg tgactatggc cccgatcaag gtgggagaca ccattccctc agtggaggta   180

tttgraggggg aacctggaaa gaaggtgaac ttggcagagc tgttcaagga caagaaaggt   240

gttttgtttg gagtccctgg ggcatttaca cctggctgtt ccaagaccca tctgcctggg   300

tttgtggagc aagccggagc tcygaaggcc aagggagcac aagtggtggc ctgtctgagt   360

gttaatgatg ycttcgtgac tgcagagtgg ggtcgagccc accaggcaga aggcaaggtt   420

cagctcctgg ctgaccccac tggagctttt ggaaaggaga cagatttact actagatgat   480

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cccaacatcc tctcacaact ctgaggccct gaccagaatg tcctctgact ctcccatctc   660

ctccacccag ctctgggcca aaggcccagt acctccttac ctgagggcca ctggaatgga   720

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            35   40   45

Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Gly Ala Xaa Lys
        50   55   60

Ala Lys Gly Ala Gln Val Val Ala Cys Leu Ser Val Asn Asp Xaa Phe
65   70   75   80

Val Thr Ala Glu Trp Gly Arg Ala His Gln Ala Glu Gly Lys Val Gln
                85   90   95

Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu Thr Asp Leu Leu
            100   105   110

Leu Asp Asp Ser Leu Val Ser Leu Phe Gly Asn Arg Arg Leu Lys Arg
            115   120   125

Phe Ser Met Val Ile Asp Lys Gly Val Val Lys Ala Leu Asn Val Glu
        130   135   140

Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro Asn Ile Leu Ser
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Gln Leu

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caggcctcac ctgcagcctg cccccaaca tcctctccca actctgaggc cctggccaga   600

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1   5   10   15

Glu Gly Glu Pro Gly Lys Lys Val Asn Leu Ala Glu Leu Phe Lys Gly
            20   25   30

Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe Thr Pro Gly Cys
        35   40   45

Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Gly Ala Leu Lys
    50   55   60

Ala Lys Gly Ala Gln Val Val Ala Cys Leu Ser Val Asn Asp Val Phe
65   70   75   80

Val Ile Glu Glu Trp Gly Arg Ala His Gln Ala Glu Gly Lys Val Arg
                85   90   95

Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Ala Thr Asp Leu Leu
            100   105   110

Leu Asp Asp Ser Leu Val Ser Leu Phe Gly Asn Arg Arg Leu Lys Arg
        115   120   125

Phe Ser Met Val Ile Asp Asn Gly Ile Val Lys Ala Leu Asn Val Glu

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              130                  135                  140
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Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro Asn Ile Leu Ser
145                  150                  155                  160
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Gln Leu
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gctggtgtcc atctttggga atcgacgtct caagaggttc tccatggtgg tacaggatgg    300

catagtgaag gccctgaatg tggaaccaga tggcacaggc ctcacctgca gcctggcacc    360

caatatcatc tcacagctct gaggccctgg gccagattac ttcctccacc cctccctatc    420

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<212> DNA
<213> Homo sapiens

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cctgccaggg tttgtggagc aggctgaggc tctgaaggcc aagggagtcc aggtggtggc    240

ctgtctgagt gttaatgatg cctttgtgac tggcgagtgg ggccgagccc acaaggcgga    300

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tgccgctgcc cttcctcttc ctcctcctga gggtgggacc ctcagacctg gccaagatcc    420

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7

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8

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9

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gaaggggagc cagggaacaa ggtgaacctg cagagctgt tcaagggcaa gaagggtgtg       300

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aatatcatct cacagctctg aggccctggg ccagattact tcctccaccc ctccctatct      720

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<400>   21

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1               5                   10                  15


Leu Val Gly Gly Ala Gly Gly Gln Ser Ala Ala Ala Ala Ala Arg Arg
            20                  25                  30


Cys Ser Glu Gly Glu Trp Ala Ser Gly Gly Val Arg Ser Phe Ser Arg
            35                  40                  45


Ala Ala Ala Ala Met Ala Pro Ile Lys Val Gly Asp Ala Ile Pro Ala
        50                  55                  60


Val Glu Val Phe Glu Gly Glu Pro Gly Asn Lys Val Asn Leu Ala Glu
65                  70                  75                  80


Leu Phe Lys Gly Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe
                85                  90                  95


Thr Pro Gly Cys Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala
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11

Glu Ala Leu Lys Ala Lys Gly Val Gln Val Val Ala Cys Leu Ser Val
        115   120   125

Asn Asp Ala Phe Val Thr Gly Glu Trp Gly Arg Ala His Lys Ala Glu
        130   135   140

Gly Lys Val Arg Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu
145   150   155   160

Thr Asp Leu Leu Leu Asp Asp Ser Leu Val Ser Ile Phe Gly Asn Arg
                165   170   175

Arg Leu Lys Arg Phe Ser Met Val Val Gln Asp Gly Ile Val Lys Ala
                180   185   190

Leu Asn Val Glu Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro
        195   200   205

Asn Ile Ile Ser Gln Leu
        210